

Raw Sequence Listing before editing (for reference only)



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/523,343

DATE: 02/10/2006
TIME: 08:48:33

Input Set : A:\21108.0021U2 Sequence Listing (Text Version).DOC
Output Set: N:\CRF4\02102006\J523343.raw

4 <110> APPLICANT: Min, Wang
5 Liu, Yingmei
7 <120> TITLE OF INVENTION: THIOREDOXIN MUTANTS AND USES THEREOF
10 <130> FILE REFERENCE: 21108.0021U2
12 <140> CURRENT APPLICATION NUMBER: 10/523,343
C--> 13 <141> CURRENT FILING DATE: 2005-02-01
15 <150> PRIOR APPLICATION NUMBER: PCT/US03/22847
16 <151> PRIOR FILING DATE: 2002-07-02
18 <150> PRIOR APPLICATION NUMBER: 60/401,073
19 <151> PRIOR FILING DATE: 2002-09-02
21 <160> NUMBER OF SEQ ID NOS: 58
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
Corrected Diskette Needed

(P3-1)

ERRORED SEQUENCES

933 <210> SEQ ID NO: 58
934 <211> LENGTH: 79
935 <212> TYPE: DNA
936 <213> ORGANISM: Artificial Sequence
938 <220> FEATURE:
939 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
940 synthetic construct
942 <400> SEQUENCE: 58
943 gatcaaaaaaa ccacggcgcc gcctccctc cgacgcccc tcaagcttca gagggcgccg 60
944 gagaggaggc ggcggcgcg 79
E--> 949 16
E--> 952 attorney dockEt nO. 21108.0021P1

→ deleted

VARIABLE LOCATION SUMMARY DATE: 02/10/2006
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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:16; Xaa Pos. 1
Seq#:17; Xaa Pos. 4
Seq#:58; N Pos. 84,90

VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:358 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:362 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:375 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:468 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:471 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:483 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:486 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:498 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:501 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:949 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:952 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:58
L:952 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:58
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:79
L:952 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:98 SEQ:58
L:952 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:952 M:112 C: (48) String data converted to lower case,
L:952 M:252 E: No. of Seq. differs, <211> LENGTH:Input:79 Found:98 SEQ:58